



## SEQUENCE LISTING

<110> Anderson, Annaliesa S.  
Montgomery, Donna L.

<120> POLYPEPTIDES FOR INDUCING A PROTECTIVE  
IMMUNE RESPONSE AGAINST STAPHYLOCOCCUS AUREUS

<130> 21490YP

<140> 10/589,381  
<141> 2006-08-15

<150> PCT/US2005/004431  
<151> 2005-02-14

<150> 60/545,447  
<151> 2004-02-18

<160> 20

<170> FastSEQ for Windows Version 4.0

<210> 1  
<211> 260  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> truncated derivative of sai-1

<400> 1  
Met Gly Thr Gln Val Ser Gln Ala Thr Ser Gln Pro Ile Asn Phe Gln  
1 5 10 15  
Val Gln Lys Asp Gly Ser Ser Glu Lys Ser His Met Asp Asp Tyr Met  
20 25 30  
Gln His Pro Gly Lys Val Ile Lys Gln Asn Asn Lys Tyr Tyr Phe Gln  
35 40 45  
Thr Val Leu Asn Asn Ala Ser Phe Trp Lys Glu Tyr Lys Phe Tyr Asn  
50 55 60  
Ala Asn Asn Gln Glu Leu Ala Thr Thr Val Val Asn Asp Asn Lys Lys  
65 70 75 80  
Ala Asp Thr Arg Thr Ile Asn Val Ala Val Glu Pro Gly Tyr Lys Ser  
85 90 95  
Leu Thr Thr Lys Val His Ile Val Val Pro Gln Ile Asn Tyr Asn His  
100 105 110  
Arg Tyr Thr Thr His Leu Glu Phe Glu Lys Ala Ile Pro Thr Leu Ala  
115 120 125  
Asp Ala Ala Lys Pro Asn Asn Val Lys Pro Val Gln Pro Lys Pro Ala  
130 135 140  
Gln Pro Lys Thr Pro Thr Glu Gln Thr Lys Pro Val Gln Pro Lys Val  
145 150 155 160  
Glu Lys Val Lys Pro Thr Val Thr Thr Ser Lys Val Glu Asp Asn  
165 170 175  
His Ser Thr Lys Val Val Ser Thr Asp Thr Thr Lys Asp Gln Thr Lys  
180 185 190  
Thr Gln Thr Ala His Thr Val Lys Thr Ala Gln Thr Ala Gln Glu Gln  
195 200 205  
Asn Lys Val Gln Thr Pro Val Lys Asp Val Ala Thr Ala Lys Ser Glu  
210 215 220

Ser Asn Asn Gln Ala Val Ser Asp Asn Lys Ser Gln Gln Thr Asn Lys  
 225 230 235 240  
 Val Thr Lys His Asn Glu Thr Pro Lys Gln Ala Ser Lys Ala Lys Glu  
 245 250 255  
 Leu Pro Lys Thr  
 260

<210> 2  
 <211> 264  
 <212> PRT  
 <213> S. aureus

&lt;220&gt;

<400> 2

Met Gly Thr Gln Val Ser Gln Ala Thr Ser Gln Pro 'Ile Asn Phe Gln  
 1 5 10 15  
 Val Gln Lys Asp Gly Ser Ser Glu Lys Ser His Met Asp Asp Tyr Met  
 20 25 30  
 Gln His Pro Gly Lys Val Ile Lys Gln Asn Asn Lys Tyr Tyr Phe Gln  
 35 40 45  
 Ala Val Leu Asn Asn Ala Ser Phe Trp Lys Glu Tyr Lys Phe Tyr Asn  
 50 55 60  
 Ala Asn Asn Gln Glu Leu Ala Thr Thr Val Val Asn Asp Asp Lys Lys  
 65 70 75 80  
 Ala Asp Thr Arg Thr Ile Asn Val Ala Val Glu Pro Gly Tyr Lys Ser  
 85 90 95  
 Leu Thr Thr Lys Val His Ile Val Val Pro Gln Ile Asn Tyr Asn His  
 100 105 110  
 Arg Tyr Thr Thr His Leu Glu Phe Glu Lys Ala Ile Pro Thr Leu Ala  
 115 120 125  
 Asp Ala Ala Lys Pro Asn Asn Val Lys Pro Val Gln Pro Lys Pro Ala  
 130 135 140  
 Gln Pro Lys Thr Pro Thr Glu Gln Thr Lys Pro Val Gln Pro Lys Val  
 145 150 155 160  
 Glu Lys Val Lys Pro Ala Val Thr Ala Pro Ser Lys Asn Glu Asn Arg  
 165 170 175  
 Gln Thr Thr Lys Val Val Ser Ser Glu Ala Thr Lys Asp Gln Ser Gln  
 180 185 190  
 Thr Gln Ser Ala Arg Thr Val Lys Thr Thr Gln Thr Ala Gln Asp Gln  
 195 200 205  
 Asn Lys Val Gln Thr Pro Val Lys Asp Val Ala Thr Ala Lys Ser Glu  
 210 215 220  
 Ser Asn Asn Gln Ala Val Ser Asp Asn Lys Ser Gln Gln Thr Asn Lys  
 225 230 235 240  
 Val Thr Lys Gln Asn Glu Val His Lys Gln Gly Pro Ser Lys Asp Ser  
 245 250 255  
 Lys Ala Lys Glu Leu Pro Lys Thr  
 260

<210> 3  
 <211> 280  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> amino His-tagged construct of SEQ ID NO: 1

<400> 3

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
 1 5 10 15

Arg Gly Ser His Met Gly Thr Gln Val Ser Gln Ala Thr Ser Gln Pro  
     20                 25                 30  
 Ile Asn Phe Gln Val Gln Lys Asp Gly Ser Ser Glu Lys Ser His Met  
     35                 40                 45  
 Asp Asp Tyr Met Gln His Pro Gly Lys Val Ile Lys Gln Asn Asn Lys  
     50                 55                 60  
 Tyr Tyr Phe Gln Thr Val Leu Asn Asn Ala Ser Phe Trp Lys Glu Tyr  
     65                 70                 75                 80  
 Lys Phe Tyr Asn Ala Asn Asn Gln Glu Leu Ala Thr Thr Val Val Asn  
     85                 90                 95  
 Asp Asn Lys Lys Ala Asp Thr Arg Thr Ile Asn Val Ala Val Glu Pro  
     100                105                110  
 Gly Tyr Lys Ser Leu Thr Thr Lys Val His Ile Val Val Pro Gln Ile  
     115                120                125  
 Asn Tyr Asn His Arg Tyr Thr Thr His Leu Glu Phe Glu Lys Ala Ile  
     130                135                140  
 Pro Thr Leu Ala Asp Ala Ala Lys Pro Asn Asn Val Lys Pro Val Gln  
     145                150                155                160  
 Pro Lys Pro Ala Gln Pro Lys Thr Pro Thr Glu Gln Thr Lys Pro Val  
     165                170                175  
 Gln Pro Lys Val Glu Lys Val Lys Pro Thr Val Thr Thr Ser Lys  
     180                185                190  
 Val Glu Asp Asn His Ser Thr Lys Val Val Ser Thr Asp Thr Thr Lys  
     195                200                205  
 Asp Gln Thr Lys Thr Gln Thr Ala His Thr Val Lys Thr Ala Gln Thr  
     210                215                220  
 Ala Gln Glu Gln Asn Lys Val Gln Thr Pro Val Lys Asp Val Ala Thr  
     225                230                235                240  
 Ala Lys Ser Glu Ser Asn Asn Gln Ala Val Ser Asp Asn Lys Ser Gln  
     245                250                255  
 Gln Thr Asn Lys Val Thr Lys His Asn Glu Thr Pro Lys Gln Ala Ser  
     260                265                270  
 Lys Ala Lys Glu Leu Pro Lys Thr  
     275                280

<210> 4  
 <211> 284  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> amino His-tagged construct of SEQ ID NO: 2

<400> 4

Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro  
     1                 5                 10                 15  
 Arg Gly Ser His Met Gly Thr Gln Val Ser Gln Ala Thr Ser Gln Pro  
     20                25                30  
 Ile Asn Phe Gln Val Gln Lys Asp Gly Ser Ser Glu Lys Ser His Met  
     35                40                45  
 Asp Asp Tyr Met Gln His Pro Gly Lys Val Ile Lys Gln Asn Asn Lys  
     50                55                60  
 Tyr Tyr Phe Gln Ala Val Leu Asn Asn Ala Ser Phe Trp Lys Glu Tyr  
     65                70                75                80  
 Lys Phe Tyr Asn Ala Asn Asn Gln Glu Leu Ala Thr Thr Val Val Asn  
     85                90                95  
 Asp Asp Lys Lys Ala Asp Thr Arg Thr Ile Asn Val Ala Val Glu Pro  
     100              105              110  
 Gly Tyr Lys Ser Leu Thr Thr Lys Val His Ile Val Val Pro Gln Ile  
     115              120              125

Asn Tyr Asn His Arg Tyr Thr Thr His Leu Glu Phe Glu Lys Ala Ile  
 130 135 140  
 Pro Thr Leu Ala Asp Ala Ala Lys Pro Asn Asn Val Lys Pro Val Gln  
 145 150 155 160  
 Pro Lys Pro Ala Gln Pro Lys Thr Pro Thr Glu Gln Thr Lys Pro Val  
 165 170 175  
 Gln Pro Lys Val Glu Lys Val Lys Pro Ala Val Thr Ala Pro Ser Lys  
 180 185 190  
 Asn Glu Asn Arg Gln Thr Thr Lys Val Val Ser Ser Glu Ala Thr Lys  
 195 200 205  
 Asp Gln Ser Gln Thr Gln Ser Ala Arg Thr Val Lys Thr Thr Gln Thr  
 210 215 220  
 Ala Gln Asp Gln Asn Lys Val Gln Thr Pro Val Lys Asp Val Ala Thr  
 225 230 235 240  
 Ala Lys Ser Glu Ser Asn Asn Gln Ala Val Ser Asp Asn Lys Ser Gln  
 245 250 255  
 Gln Thr Asn Lys Val Thr Lys Gln Asn Glu Val His Lys Gln Gly Pro  
 260 265 270  
 Ser Lys Asp Ser Lys Ala Lys Glu Leu Pro Lys Thr  
 275 280

<210> 5

<211> 268

<212> PRT

<213> Artificial Sequence

<220>

<223> carboxyl His-tagged construct of SEQ ID NO: 1

<400> 5

Met Gly Thr Gln Val Ser Gln Ala Thr Ser Gln Pro Ile Asn Phe Gln  
 1 5 10 15  
 Val Gln Lys Asp Gly Ser Ser Glu Lys Ser His Met Asp Asp Tyr Met  
 20 25 30  
 Gln His Pro Gly Lys Val Ile Lys Gln Asn Asn Lys Tyr Tyr Phe Gln  
 35 40 45  
 Thr Val Leu Asn Asn Ala Ser Phe Trp Lys Glu Tyr Lys Phe Tyr Asn  
 50 55 60  
 Ala Asn Asn Gln Glu Leu Ala Thr Thr Val Val Asn Asp Asn Lys Lys  
 65 70 75 80  
 Ala Asp Thr Arg Thr Ile Asn Val Ala Val Glu Pro Gly Tyr Lys Ser  
 85 90 95  
 Leu Thr Thr Lys Val His Ile Val Val Pro Gln Ile Asn Tyr Asn His  
 100 105 110  
 Arg Tyr Thr Thr His Leu Glu Phe Glu Lys Ala Ile Pro Thr Leu Ala  
 115 120 125  
 Asp Ala Ala Lys Pro Asn Asn Val Lys Pro Val Gln Pro Lys Pro Ala  
 130 135 140  
 Gln Pro Lys Thr Pro Thr Glu Gln Thr Lys Pro Val Gln Pro Lys Val  
 145 150 155 160  
 Glu Lys Val Lys Pro Thr Val Thr Thr Ser Lys Val Glu Asp Asn  
 165 170 175  
 His Ser Thr Lys Val Val Ser Thr Asp Thr Thr Lys Asp Gln Thr Lys  
 180 185 190  
 Thr Gln Thr Ala His Thr Val Lys Thr Ala Gln Thr Ala Gln Glu Gln  
 195 200 205  
 Asn Lys Val Gln Thr Pro Val Lys Asp Val Ala Thr Ala Lys Ser Glu  
 210 215 220  
 Ser Asn Asn Gln Ala Val Ser Asp Asn Lys Ser Gln Gln Thr Asn Lys  
 225 230 235 240

Val	Thr	Lys	His	Asn	Glu	Thr	Pro	Lys	Gln	Ala	Ser	Lys	Ala	Lys	Glu
					245				250					255	
Leu	Pro	Lys	Thr	Leu	Glu	His									
					260				265						

<210> 6  
<211> 395  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> amino His-tagged construct of SEQ ID NO: 7

<400> 6																
Met	His	His	His	His	His	Ser	Ser	Gly	Leu	Val	Pro	Arg	Gly	Ser		
						5			10					15		
Gly	Met	Lys	Glu	Thr	Ala	Ala	Ala	Lys	Phe	Glu	Arg	Gln	His	Met	Asp	
						20			25					30		
Ser	Pro	Asp	Leu	Gly	Thr	Asp	Asp	Asp	Lys	Ala	Met	Gly	Thr	Lys		
						35			40				45			
His	Tyr	Leu	Asn	Ser	Lys	Tyr	Gln	Ser	Glu	Gln	Arg	Ser	Ser	Ala	Met	
						50			55				60			
Lys	Lys	Ile	Thr	Met	Gly	Thr	Ala	Ser	Ile	Ile	Leu	Gly	Ser	Leu	Val	
						65			70				75			80
Tyr	Ile	Gly	Ala	Asp	Ser	Gln	Gln	Val	Asn	Ala	Ala	Thr	Glu	Ala	Thr	
						85			90				95			
Asn	Ala	Thr	Asn	Asn	Gln	Ser	Thr	Gln	Val	Ser	Gln	Ala	Thr	Ser	Gln	
						100			105				110			
Pro	Ile	Asn	Phe	Gln	Val	Gln	Lys	Asp	Gly	Ser	Ser	Glu	Lys	Ser	His	
						115			120				125			
Met	Asp	Asp	Tyr	Met	Gln	His	Pro	Gly	Lys	Val	Ile	Lys	Gln	Asn	Asn	
						130			135				140			
Lys	Tyr	Tyr	Phe	Gln	Thr	Val	Leu	Asn	Ala	Ser	Phe	Trp	Lys	Glu		
						145			150				155			160
Tyr	Lys	Phe	Tyr	Asn	Ala	Asn	Asn	Gln	Glu	Leu	Ala	Thr	Thr	Val	Val	
						165			170				175			
Asn	Asp	Asn	Lys	Lys	Ala	Asp	Thr	Arg	Thr	Ile	Asn	Val	Ala	Val	Glu	
						180			185				190			
Pro	Gly	Tyr	Lys	Ser	Leu	Thr	Thr	Lys	Val	His	Ile	Val	Val	Pro	Gln	
						195			200				205			
Ile	Asn	Tyr	Asn	His	Arg	Tyr	Thr	Thr	His	Leu	Glu	Phe	Glu	Lys	Ala	
						210			215				220			
Ile	Pro	Thr	Leu	Ala	Asp	Ala	Ala	Lys	Pro	Asn	Asn	Val	Lys	Pro	Val	
						225			230				235			240
Gln	Pro	Lys	Pro	Ala	Gln	Pro	Lys	Thr	Pro	Thr	Glu	Gln	Thr	Lys	Pro	
						245			250				255			
Val	Gln	Pro	Lys	Val	Glu	Lys	Val	Lys	Pro	Thr	Val	Thr	Thr	Thr	Ser	
						260			265				270			
Lys	Val	Glu	Asp	Asn	His	Ser	Thr	Lys	Val	Val	Ser	Thr	Asp	Thr	Thr	
						275			280				285			
Lys	Asp	Gln	Thr	Lys	Thr	Gln	Thr	Ala	His	Thr	Val	Lys	Thr	Ala	Gln	
						290			295				300			
Thr	Ala	Gln	Glu	Gln	Asn	Lys	Val	Gln	Thr	Pro	Val	Lys	Asp	Val	Ala	
						305			310				315			320
Thr	Ala	Lys	Ser	Glu	Ser	Asn	Asn	Gln	Ala	Val	Ser	Asp	Asn	Lys	Ser	
						325			330				335			
Gln	Gln	Thr	Asn	Lys	Val	Thr	Lys	His	Asn	Glu	Thr	Pro	Lys	Gln	Ala	
						340			345				350			
Ser	Lys	Ala	Lys	Glu	Leu	Pro	Lys	Thr	Gly	Leu	Thr	Ser	Val	Asp	Asn	
						355			360				365			

Phe Ile Ser Thr Val Ala Phe Ala Thr Leu Ala Leu Leu Gly Ser Leu  
 370 375 380  
 Ser Leu Leu Leu Phe Lys Arg Lys Glu Ser Lys  
 385 390 395

<210> 7  
 <211> 350  
 <212> PRT  
 <213> S. aureus

<400> 7  
 Met Thr Lys His Tyr Leu Asn Ser Lys Tyr Gln Ser Glu Gln Arg Ser  
 1 5 10 15  
 Ser Ala Met Lys Lys Ile Thr Met Gly Thr Ala Ser Ile Ile Leu Gly  
 20 25 30  
 Ser Leu Val Tyr Ile Gly Ala Asp Ser Gln Gln Val Asn Ala Ala Thr  
 35 40 45  
 Glu Ala Thr Asn Ala Thr Asn Asn Gln Ser Thr Gln Val Ser Gln Ala  
 50 55 60  
 Thr Ser Gln Pro Ile Asn Phe Gln Val Gln Lys Asp Gly Ser Ser Glu  
 65 70 75 80  
 Lys Ser His Met Asp Asp Tyr Met Gln His Pro Gly Lys Val Ile Lys  
 85 90 95  
 Gln Asn Asn Lys Tyr Tyr Phe Gln Thr Val Leu Asn Asn Ala Ser Phe  
 100 105 110  
 Trp Lys Glu Tyr Lys Phe Tyr Asn Ala Asn Asn Gln Glu Leu Ala Thr  
 115 120 125  
 Thr Val Val Asn Asp Asn Lys Lys Ala Asp Thr Arg Thr Ile Asn Val  
 130 135 140  
 Ala Val Glu Pro Gly Tyr Lys Ser Leu Thr Thr Lys Val His Ile Val  
 145 150 155 160  
 Val Pro Gln Ile Asn Tyr Asn His Arg Tyr Thr Thr His Leu Glu Phe  
 165 170 175  
 Glu Lys Ala Ile Pro Thr Leu Ala Asp Ala Ala Lys Pro Asn Asn Val  
 180 185 190  
 Lys Pro Val Gln Pro Lys Pro Ala Gln Pro Lys Thr Pro Thr Glu Gln  
 195 200 205  
 Thr Lys Pro Val Gln Pro Lys Val Glu Lys Val Lys Pro Thr Val Thr  
 210 215 220  
 Thr Thr Ser Lys Val Glu Asp Asn His Ser Thr Lys Val Val Ser Thr  
 225 230 235 240  
 Asp Thr Thr Lys Asp Gln Thr Lys Thr Gln Thr Ala His Thr Val Lys  
 245 250 255  
 Thr Ala Gln Thr Ala Gln Glu Gln Asn Lys Val Gln Thr Pro Val Lys  
 260 265 270  
 Asp Val Ala Thr Ala Lys Ser Glu Ser Asn Asn Gln Ala Val Ser Asp  
 275 280 285  
 Asn Lys Ser Gln Gln Thr Asn Lys Val Thr Lys His Asn Glu Thr Pro  
 290 295 300  
 Lys Gln Ala Ser Lys Ala Lys Glu Leu Pro Lys Thr Gly Leu Thr Ser  
 305 310 315 320  
 Val Asp Asn Phe Ile Ser Thr Val Ala Phe Ala Thr Leu Ala Leu Leu  
 325 330 335  
 Gly Ser Leu Ser Leu Leu Leu Phe Lys Arg Lys Glu Ser Lys  
 340 345 350

<210> 8  
 <211> 354  
 <212> PRT  
 <213> S. aureus

<400> 8

Met Thr Lys His Tyr Leu Asn Ser Lys Tyr Gln Ser Glu Gln Arg Ser  
 1 5 10 15  
 Ser Ala Met Lys Lys Ile Thr Met Gly Thr Ala Ser Ile Ile Leu Gly  
 20 25 30  
 Ser Leu Val Tyr Ile Gly Ala Asp Ser Gln Gln Val Asn Ala Ala Thr  
 35 40 45  
 Glu Ala Thr Asn Ala Thr Asn Asn Gln Ser Thr Gln Val Ser Gln Ala  
 50 55 60  
 Thr Ser Gln Pro Ile Asn Phe Gln Val Gln Lys Asp Gly Ser Ser Glu  
 65 70 75 80  
 Lys Ser His Met Asp Asp Tyr Met Gln His Pro Gly Lys Val Ile Lys  
 85 90 95  
 Gln Asn Asn Lys Tyr Tyr Phe Gln Ala Val Leu Asn Asn Ala Ser Phe  
 100 105 110  
 Trp Lys Glu Tyr Lys Phe Tyr Asn Ala Asn Asn Gln Glu Leu Ala Thr  
 115 120 125  
 Thr Val Val Asn Asp Asp Lys Lys Ala Asp Thr Arg Thr Ile Asn Val  
 130 135 140  
 Ala Val Glu Pro Gly Tyr Lys Ser Leu Thr Thr Lys Val His Ile Val  
 145 150 155 160  
 Val Pro Gln Ile Asn Tyr Asn His Arg Tyr Thr Thr His Leu Glu Phe  
 165 170 175  
 Glu Lys Ala Ile Pro Thr Leu Ala Asp Ala Ala Lys Pro Asn Asn Val  
 180 185 190  
 Lys Pro Val Gln Pro Lys Pro Ala Gln Pro Lys Thr Pro Thr Glu Gln  
 195 200 205  
 Thr Lys Pro Val Gln Pro Lys Val Glu Lys Val Lys Pro Ala Val Thr  
 210 215 220  
 Ala Pro Ser Lys Asn Glu Asn Arg Gln Thr Thr Lys Val Val Ser Ser  
 225 230 235 240  
 Glu Ala Thr Lys Asp Gln Ser Gln Thr Gln Ser Ala Arg Thr Val Lys  
 245 250 255  
 Thr Thr Gln Thr Ala Gln Asp Gln Asn Lys Val Gln Thr Pro Val Lys  
 260 265 270  
 Asp Val Ala Thr Ala Lys Ser Glu Ser Asn Asn Gln Ala Val Ser Asp  
 275 280 285  
 Asn Lys Ser Gln Gln Thr Asn Lys Val Thr Lys Gln Asn Glu Val His  
 290 295 300  
 Lys Gln Gly Pro Ser Lys Asp Ser Lys Ala Lys Glu Leu Pro Lys Thr  
 305 310 315 320  
 Gly Leu Thr Ser Val Asp Asn Phe Ile Ser Thr Val Ala Phe Ala Thr  
 325 330 335  
 Leu Ala Leu Leu Gly Ser Leu Ser Leu Leu Leu Phe Lys Arg Lys Glu  
 340 345 350  
 Ser Lys

<210> 9  
 <211> 358  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> carboxyl His-tagged construct of SEQ ID NO: 7

<400> 9

Met Thr Lys His Tyr Leu Asn Ser Lys Tyr Gln Ser Glu Gln Arg Ser  
 1 5 10 15  
 Ser Ala Met Lys Lys Ile Thr Met Gly Thr Ala Ser Ile Ile Leu Gly  
 20 25 30

Ser Leu Val Tyr Ile Gly Ala Asp Ser Gln Gln Val Asn Ala Ala Thr  
 35 40 45  
 Glu Ala Thr Asn Ala Thr Asn Asn Gln Ser Thr Gln Val Ser Gln Ala  
 50 55 60  
 Thr Ser Gln Pro Ile Asn Phe Gln Val Gln Lys Asp Gly Ser Ser Glu  
 65 70 75 80  
 Lys Ser His Met Asp Asp Tyr Met Gln His Pro Gly Lys Val Ile Lys  
 85 90 95  
 Gln Asn Asn Lys Tyr Tyr Phe Gln Thr Val Leu Asn Asn Ala Ser Phe  
 100 105 110  
 Trp Lys Glu Tyr Lys Phe Tyr Asn Ala Asn Asn Gln Glu Leu Ala Thr  
 115 120 125  
 Thr Val Val Asn Asp Asn Lys Lys Ala Asp Thr Arg Thr Ile Asn Val  
 130 135 140  
 Ala Val Glu Pro Gly Tyr Lys Ser Leu Thr Thr Lys Val His Ile Val  
 145 150 155 160  
 Val Pro Gln Ile Asn Tyr Asn His Arg Tyr Thr Thr His Leu Glu Phe  
 165 170 175  
 Glu Lys Ala Ile Pro Thr Leu Ala Asp Ala Ala Lys Pro Asn Asn Val  
 180 185 190  
 Lys Pro Val Gln Pro Lys Pro Ala Gln Pro Lys Thr Pro Thr Glu Gln  
 195 200 205  
 Thr Lys Pro Val Gln Pro Lys Val Glu Lys Val Lys Pro Thr Val Thr  
 210 215 220  
 Thr Thr Ser Lys Val Glu Asp Asn His Ser Thr Lys Val Val Ser Thr  
 225 230 235 240  
 Asp Thr Thr Lys Asp Gln Thr Lys Thr Gln Thr Ala His Thr Val Lys  
 245 250 255  
 Thr Ala Gln Thr Ala Gln Glu Gln Asn Lys Val Gln Thr Pro Val Lys  
 260 265 270  
 Asp Val Ala Thr Ala Lys Ser Glu Ser Asn Asn Gln Ala Val Ser Asp  
 275 280 285  
 Asn Lys Ser Gln Gln Thr Asn Lys Val Thr Lys His Asn Glu Thr Pro  
 290 295 300  
 Lys Gln Ala Ser Lys Ala Lys Glu Leu Pro Lys Thr Gly Leu Thr Ser  
 305 310 315 320  
 Val Asp Asn Phe Ile Ser Thr Val Ala Phe Ala Thr Leu Ala Leu Leu  
 325 330 335  
 Gly Ser Leu Ser Leu Leu Phe Lys Arg Lys Glu Ser Lys Leu Glu  
 340 345 350  
 His His His His His  
 355

&lt;210&gt; 10

&lt;211&gt; 843

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; nucleic acid sequence encoding SEQ ID NO: 3

&lt;400&gt; 10

atgggcagca gcccatacatca tcatacatcac agcagcggcc tggtgccgcg cggcagccat 60  
 atgggcacac aagtttctca agcaacatca caaccaatta atttccaagt gcaaaaaagat 120  
 ggctttaga agaagtaca catggatgac tatatgcaac accctgttaa agtaattaaa 180  
 caaaaataata aatatttattt ccaaaccgtg ttaaaacaatg catcatctg gaaagaatac 240  
 aaattttaca atgcaaacaa tcaagaatata gcaacaactg ttgttaacga taataaaaaaa 300  
 gcgatataca gaacaatcaa tggtgcaattt gaaacctggat ataagagctt aactactaaa 360  
 gtacatattt tcgtgccaca aattaattac aatcatagat atactacgca ttggaaattt 420  
 gaaaaagcaa ttcctacatt agctgacgca gcaaaaaccaa acaatgttaa accggttcaa 480  
 ccaaaaaccag ctcaacctaa aacacctact gagcaaacta aaccagttca acctaaagtt 540

gaaaaagtt aacctactgt aactacaaca agcaaagttg aagacaatca ctctactaaa 600  
 gttgtaagta ctgacacaac aaaagatcaa actaaaacac aaactgctca tacagttaaa 660  
 acagcacaaa ctgctcaaga acaaaaataaa gttcaaacac ctgttaaaga tggcaaca 720  
 gcgaaatctg aaagcaacaa tcaagctgt agtgataata aatcacaaca aactaacaaa 780  
 gttacaaaac ataacgaaac gcctaaacaa gcatctaaag ctaaagaatt accaaaaact 840  
 tga 843

<210> 11  
 <211> 855  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> nucleic acid sequence encoding SEQ ID NO: 4

<400> 11  
 atggcagca gccatcatca tcatacatcac agcagcggcc tggtgccgcg cgccagccat 60  
 atggcacaac aagttctca agcaacatca caaccaatta atttccaagt gcaaaaagat 120  
 ggctcttcag agaagtcaca catggatgac tatatgcaac accctgtaa agtgattaaa 180  
 caaaaataata aatattattt ccaagctgtt ttgaacaacg catcattctg gaaagaatac 240  
 aaattttaca atgcaacaa tcaagaatata gcaacaactg ttgttaacga tgataaaaaaa 300  
 gctgacacta gaacaatcaa tggctgtt gaacctgggt ataagagttt aactacaaaaa 360  
 gtacatattt tcgtgccaca aattaattat aatcatagat atactacgca tttagaattt 420  
 gaaaaagcaa ttcctacatt agctgacgca gcaaaaaccaa acaatgttaa accggttcaa 480  
 ccaaaacctg ctcaacctaa aacacctact gagcaaacga aaccaggta acctaaagtt 540  
 gaaaaagtt aacctgctgt aactgcacca agcaaaaatg aaaacagaca aactacaaaaa 600  
 gttgtaagta gtgaagctac aaaagatcaa agtcaaacac aaagtgcctg tacagtgaaa 660  
 acaacacacaa cagctcaaga tcaaaaataaa gttcaaacac ctgttaaaga tggcaaca 720  
 gcgaaatctg aaagcaacaa tcaagctgtt agtgacaata aatcacaaca aactaacaaa 780  
 gttacaaaac aaaacaaatgt tcataaacaa ggaccttcaa aagattctaa agctaaagaa 840  
 ttacaaaaaa cttga 855

<210> 12  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 12  
 gagatataacc atgggcacaa aacattattt aaacagt

37

<210> 13  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 13  
 ccggcggccc tcgagtttag attctttct tttgaa

36

<210> 14  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 14		
gagatataacc atgggcacaa aacattattt aaacagt		37
<210> 15		
<211> 39		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> primer		
<400> 15		
ccggcgcccc tcgagttatt tagattcttt tctttgaa		39
<210> 16		
<211> 41		
<212> DNA		
<213> Artificial Sequence		
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<223> primer		
<400> 16		
gagatataacc atgggcacac aagtttctca agcaacatca c		41
<210> 17		
<211> 36		
<212> DNA		
<213> Artificial Sequence		
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